

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/881,853

TIME: 11:11:57

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07032001\I881853.raw

3 <110> APPLICANT: YIN, AMY
 4 MIRAGLIA, SHERI
 5 GODFREY, WAYNE
 6 BUCK, DAVID
 8 <120> TITLE OF INVENTION: HUMAN HEMTOPOIETIC STEM AND PROGENITOR CELL ANTIGEN AND
 METHODS FOR ITS
 9 USE
 11 <130> FILE REFERENCE: AMCE-012/02US
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/881,853
 C--> 13 <141> CURRENT FILING DATE: 2001-06-13
 13 <150> PRIOR APPLICATION NUMBER: 08/842,382
 14 <151> PRIOR FILING DATE: 1997-04-23
 16 <150> PRIOR APPLICATION NUMBER: 08/639,891
 17 <151> PRIOR FILING DATE: 1996-04-26
 19 <160> NUMBER OF SEQ ID NOS: 2
 21 <170> SOFTWARE: PatentIn version 3.0
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 24 <211> LENGTH: 3804
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (38)..(2632)
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 35 1 5
 37 tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag 103
 38 Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
 39 10 15 20
 41 cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca 151
 42 Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
 43 25 30 35
 45 aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att 199
 46 Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
 47 40 45 50
 49 ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat 247
 50 Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
 51 55 60 65 70
 53 ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc 295
 54 Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
 55 75 80 85
 57 aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att 343
 58 Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
 59 90 95 100
 61 gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg 391
 62 Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
 63 105 110 115

ENTERED

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69	tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat	487
70	Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn	
71	135 140 145 150	
73	ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt	535
74	Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys	
75	155 160 165	
77	ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag	583
78	Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln	
79	170 175 180	
81	gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc	631
82	Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe	
83	185 190 195	
85	aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat	679
86	Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr	
87	200 205 210	
89	ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg	727
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91	215 220 225 230	
93	aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga	775
94	Asn Ser Ile Asn Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg	
95	235 240 245	
97	ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gcg	823
98	Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala	
99	250 255 260	
101	atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag	871
102	Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys	
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105	agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gtg	919
106	Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val	
107	280 285 290	
109	aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat	967
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111	295 300 305 310	
113	cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg	1015
114	Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu	
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117	aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt	1063
118	Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu	
119	330 335 340	
121	gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa	1111
122	Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln	
123	345 350 355	
125	cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa	1159
126	Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln	
127	360 365 370	
129	acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt	1207

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134	Ser	Asp	Ile	Asp	Asn	Val	Thr	Gln	Arg	Leu	Pro	Ile	Gln	Asp	Ile	Leu	
135					395					400					405		
137	tca	gca	ttc	tct	gtt	tat	gtt	aat	aac	act	gaa	agt	tac	atc	cac	aga	1303
138	Ser	Ala	Phe	Ser	Val	Tyr	Val	Asn	Asn	Thr	Glu	Ser	Tyr	Ile	His	Arg	
139				410					415					420			
141	aat	tta	cct	aca	ttg	gaa	gag	tat	gat	tca	tac	tggt	tggt	ctg	ggt	ggc	1351
142	Asn	Leu	Pro	Thr	Leu	Glu	Glu	Tyr	Asp	Ser	Tyr	Trp	Trp	Leu	Gly	Gly	
143			425					430					435				
145	ctg	gtc	atc	tgc	tct	ctg	ctg	acc	ctc	atc	gtg	att	ttt	tac	tac	ctg	1399
146	Leu	Val	Ile	Cys	Ser	Leu	Leu	Thr	Leu	Ile	Val	Ile	Phe	Tyr	Tyr	Leu	
147		440				445						450					
149	ggc	tta	ctg	tgt	ggc	gtg	tgc	ggc	tat	gac	agg	cat	gcc	acc	ccg	acc	1447
150	Gly	Leu	Leu	Cys	Gly	Val	Cys	Gly	Tyr	Asp	Arg	His	Ala	Thr	Pro	Thr	
151	455				460					465					470		
153	acc	cga	ggc	tgt	gtc	tcc	aac	acc	gga	ggc	gtc	ttc	ctc	atg	gtt	gga	1495
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155				475						480					485		
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159			490						495					500			
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162	Leu	Thr	Phe	Val	Phe	Gly	Ala	Asn	Val	Glu	Lys	Leu	Ile	Cys	Glu	Pro	
163			505					510					515				
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167		520				525						530					
169	aat	gaa	gac	tgg	gaa	tac	tat	ctc	tct	ggg	aag	cta	ttt	aat	aaa	tca	1687
170	Asn	Glu	Asp	Trp	Glu	Tyr	Tyr	Leu	Ser	Gly	Lys	Leu	Phe	Asn	Lys	Ser	
171	535				540					545					550		
173	aaa	atg	aag	ctc	act	ttt	gaa	caa	gtt	tac	agt	gac	tgc	aaa	aaa	aat	1735
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175				555						560					565		
177	aga	ggc	act	tac	ggc	act	ctt	cac	ctg	cag	aac	agc	ttc	aat	atc	agt	1783
178	Arg	Gly	Thr	Tyr	Gly	Thr	Leu	His	Leu	Gln	Asn	Ser	Phe	Asn	Ile	Ser	
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181	gaa	cat	ctc	aac	att	aat	gag	cat	act	gga	agc	ata	agc	agt	gaa	ttg	1831
182	Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly	Ser	Ile	Ser	Ser	Glu	Leu	
183			585					590					595				
185	gaa	agt	ctg	aag	gta	aat	ctt	aat	atc	ttt	ctg	ttg	ggg	gca	gca	gga	1879
186	Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe	Leu	Leu	Gly	Ala	Ala	Gly	
187		600				605						610					
189	aga	aaa	aac	ctt	cag	gat	ttt	gct	gct	tgt	gga	ata	gac	aga	atg	aat	1927
190	Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys	Gly	Ile	Asp	Arg	Met	Asn	
191	615				620						625				630		
193	tat	gac	agc	tac	ttg	gct	cag	act	ggg	aaa	tcc	ccc	gca	gga	gtg	aat	1975
194	Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys	Ser	Pro	Ala	Gly	Val	Asn	

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201	cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa							2071
202	Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys							
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206	Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr							
207		680		685		690		
209	cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg							2167
210	Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu							
211	695		700		705		710	
213	gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc							2215
214	Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe							
215		715		720		725		
217	atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat							2263
218	Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr							
219		730		735		740		
221	ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag							2311
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226	Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala							
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234	Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu							
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237	ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg							2503
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243		825		830		835		
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255	tacaaggact ttccaaatcc aggagcaacg ccagtggcaa cgtagtgact caggcgggca							2772
257	ccaaggcaac ggcaccattg gtctctgggt agtgcttttaaatgaacac aatcacgtta							2832
259	tagtccatgg tccatcacta ttcaaggatg actccctccc ttcctgtcta tttttgtttt							2892
261	ttactttttt aactgagtt tctatttaga cactacaaca tatggggtgt ttgttcccat							2952
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269 cttctaaatg agctaaataa gtcaccattg acttcttggt gctgttgaaa ataatccatt 3192
271 ttcactaaaa gtgtgtgaaa cctacagcat attcttcacg cagagatttt catctattat 3252
273 actttatcaa agattggcca tgttccactt ggaaatggca tgcaaaagcc atcatagaga 3312
275 aacctgcgta actccatctg acaaattcaa aagagagaga gagatcttga gagagaaatg 3372
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279 agttttctgt tgcattagga taaacattaa ttggagtgcg gctaacaatga gtatcatcag 3492
281 actagtatca agtgttctaa aatgaaatat gagaagatcc tgtcacaatt cttagatctg 3552
283 gtgtccagca tggatgaaac ctttgagttt ggtccctaaa tttgcatgaa agcacaaggt 3612
285 aaatattcat ttgcttcagg agtttcatgt tggatctgtc attatcaaaa gtgatcagca 3672
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309 Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys
310 35 40 45
313 Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr
314 50 55 60
317 Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu
318 65 70 75 80
321 Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val
322 85 90 95
325 Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys
326 100 105 110
329 Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr
330 115 120 125
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342 165 170 175
345 Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys
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350 195 200 205
353 Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp
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357 Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly Gly
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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date